



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lee, Jong Y.
- (ii) TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Fish & Richardson P.C., P.A.
  - (B) STREET: 60 South Sixth Street, Suite 3300
  - (C) CITY: Minneapolis
  - (D) STATE: MN
  - (E) COUNTRY: USA
  - (F) ZIP: 55402
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM compatible
  - (C) OPERATING SYSTEM: DOS
  - (D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: 09/016,159
  - (B) FILING DATE: 30-JAN-1998
- (vi) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/876,227
  - (B) FILING DATE: 16-JUN-1997
- (vi) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/734,097
  - (B) FILING DATE: 21-OCT-1996
- (vi) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/460,525
  - (B) FILING DATE: 02-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Ellinger, Mark S.
  - (B) REGISTRATION NUMBER: 34,812
  - (C) REFERENCE/DOCKET NUMBER: 07004/002003
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 612/335-5070
  - (B) TELEFAX: 612/288-9696

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 23 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: BamH1 linker at 5' end followed by sequence for amino acids 25 through 29 of the full length human Epor protein. Forward primer for Sequence ID No. 2."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGATCC GCG CCC CCG CCT A AC  
Ala Pro Pro Pro  
1

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: synthetic DNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: EcoR1 linker followed by sequence complementary to coding sequence for amino acids 226 through 222 of full length human Epor protein. Reverse primer for Sequence ID No. 1.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

TGAATTCGGG GTCCAGGTCTG CT

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(vii) IMMEDIATE SOURCE:

(B) CLONE: pGEX-2T, Pharmacia (Mechanicsburg, PA)

(ix) FEATURE:

(A) NAME/KEY: Thrombin Cleavage Site in plasmid vector pGEX-2T."

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Smith, D.B.  
Johnson, K.S.

(B) TITLE: Single-step purification of polypeptides  
expressed in Escherichia coli as fusions with  
glutathione-S-transferase

(D) VOLUME: 67

(F) PAGES: 31-40

(G) DATE: 1988

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTG GTT CCG CGT GGA T CC  
Leu Val Pro Arg Gly  
5

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1527 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Winkelmann, J. C., et al.  
(C) JOURNAL: Blood  
(D) VOLUME: 76  
(E) ISSUE: 1  
(F) PAGES: 24-30  
(G) DATE: 1990

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Jones, S.S., et al.  
(C) JOURNAL: Blood  
(D) VOLUME: 76  
(E) ISSUE: 1  
(F) PAGES: 31-35  
(G) DATE: 1990

(x) PUBLICATION INFORMATION:

(A) AUTHORS: Noguchi, C.T., et al.  
(C) JOURNAL: Blood  
(D) VOLUME: 78  
(E) ISSUE: 10  
(F) PAGES: 2548-2556  
(G) DATE: 1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG GAC CAC CTC GGG GCG TCC CTC TGG CCC CAG GTC GGC TCC CTT TGT  
Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys  
1 5 10 15

48

CTC CTG CTC GCT GGG GCC GCC TGG GCG CCC CCG CCT AAC CTC CCG GAC  
Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp  
20 25 30

96

CCC AAG TTC GAG AGC AAA GCG GCC TTG CTG GCG GCC CGG GGG CCC GAA  
Pro Lys Phe Glu Ser Lys Ala Ala Leu Ala Ala Arg Gly Pro Glu

144

35	40	45	
GAG CTT CTG TGC TTC ACC GAG CGG TTG GAG GAC TTG GTG TGT TTC TGG Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp 50 55 60			192
GAG GAA GCG GCG AGC GCT GGG GTG GGC CCG GGC AAC TAC AGC TTC TCC Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser 65 70 75 80			240
TAC CAG CTC GAG GAT GAG CCA TGG AAG CTG TGT CGC CTG CAC CAG GCT Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala 85 90 95			288
CCC ACG GCT CGT GGT GCG GTG CGC TTC TGG TGT TCG CTG CCT ACA GCC Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala 100 105 110			336
GAC ACG TCG AGC TTC GTG CCC CTA GAG TTG CGC GTC ACA GCA GCC TCC Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser 115 120 125			384
GGC GCT CCG CGA TAT CAC CGT GTC ATC CAC ATC AAT GAA GTA GTG CTC Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu 130 135 140			432
CTA GAC GCC CCC GTG GGG CTG GTG GCG CGG TTG GCT GAC GAG AGC GGC Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly 145 150 155 160			480
CAC GTA GTG TTG CGC TGG CTC CCG CCG CCT GAG ACA CCC ATG ACG TCT His Val Val Leu Arg Trp Leu Pro Pro Glu Thr Pro Met Thr Ser 165 170 175			528
CAC ATC CGC TAC GAG GTG GAC GTC TCG GCC GGC AAC GGC GCA GGG AGC His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser 180 185 190			576
GTA CAG AGG GTG GAG ATC CTG GAG GGC CGC ACC GAG TGT GTG CTG AGC Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser 195 200 205			624
AAC CTG CGG GGC CGG ACG CGC TAC ACC TTC GCC GTC CTC GCG CGT ATG Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Leu Ala Arg Met 210 215 220			672
GCT GAG CCG AGC TTC GGC GGC TTC TGG AGC GCC TGG TCG GAG CCT GTG Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val 225 230 235 240			720
TCG CTG CTG ACG CCT AGC GAC CTG GAC CCC CTC ATC CTG ACG CTC TCC Ser Leu Leu Thr Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser 245 250 255			768
CTC ATC CTC GTG GTC ATC CTG GTG CTG CTG ACC GTG CTC GCG CTG CTC Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu 260 265 270			816
TCC CAC CGC CGG GCT CTG AAG CAG AAG ATC TGG CCT GGC ATC CCG AGC Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser 275 280 285			864

CCA GAG AGC GAG TTT GAA GGC CTC TTC ACC ACC CAC AAG GGT AAC TTC Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe 290 295 300	912
CAG CTG TGG CTG TAC CAG AAT GAT GGC TGC CTG TGG TGG AGC CCC TGC Gln Leu Trp Leu Tyr Gln Asn Asp Gly Cys Leu Trp Trp Ser Pro Cys 305 310 315 320	960
ACC CCC TTC ACG GAG GAC CCA CCT GCT TCC CTG GAA GTC CTC TCA GAG Thr Pro Phe Thr Glu Asp Pro Pro Ala Ser Leu Glu Val Leu Ser Glu 325 330 335	1008
CGC TGC TGG GGG ACG ATG CAG GCA GTG GAG CCG GGG ACA GAT GAT GAG Arg Cys Trp Gly Thr Met Gln Ala Val Glu Pro Gly Thr Asp Asp Glu 340 345 350	1056
GGC CCC CTG CTG GAG CCA GTG GGC AGT GAG CAT GCC CAG GAT ACC TAT Gly Pro Leu Leu Glu Pro Val Gly Ser Glu His Ala Gln Asp Thr Tyr 355 360 365	1104
CTG GTG CTG GAC AAA TGG TTG CTG CCC CGG AAC CCG CCC AGT GAG GAC Leu Val Leu Asp Lys Trp Leu Leu Pro Arg Asn Pro Pro Ser Glu Asp 370 375 380	1152
CTC CCA GGG CCT GGT GGC AGT GTG GAC ATA GTG GCC ATG GAT GAA GGC Leu Pro Gly Pro Gly Ser Val Asp Ile Val Ala Met Asp Glu Gly 385 390 395 400	1200
TCA GAA GCA TCC TCC TGC TCA TCT GCT TTG GCC TCG AAG CCC AGC CCA Ser Glu Ala Ser Ser Cys Ser Ala Leu Ala Ser Lys Pro Ser Pro 405 410 415	1248
GAG GGA GCC TCT GCT GCC AGC TTT GAG TAC ACT ATC CTG GAC CCC AGC Glu Gly Ala Ser Ala Ala Ser Phe Glu Tyr Thr Ile Leu Asp Pro Ser 420 425 430	1296
TCC CAG CTC TTG CGT CCA TGG ACA CTG TGC CCT GAG CTG CCC CCT ACC Ser Gln Leu Leu Arg Pro Trp Thr Leu Cys Pro Glu Leu Pro Pro Thr 435 440 445	1344
CCA CCC CAC CTA AAG TAC CTG TAC CTT GTG GTA TCT GAC TCT GGC ATC Pro Pro His Leu Lys Tyr Leu Tyr Leu Val Val Ser Asp Ser Gly Ile 450 455 460	1392
TCA ACT GAC TAC AGC TCA GGG GAC TCC CAG GGA GCC CAA GGG GGC TTA Ser Thr Asp Tyr Ser Ser Gly Asp Ser Gln Gly Ala Gln Gly Gly Leu 465 470 475 480	1440
TCC GAT GGC CCC TAC TCC AAC CCT TAT GAG AAC AGC CTT ATC CCA GCC Ser Asp Gly Pro Tyr Ser Asn Pro Tyr Glu Asn Ser Leu Ile Pro Ala 485 490 495	1488
GCT GAG CCT CTG CCC CCC AGC TAT GTG GCT TGC TCT TAG Ala Glu Pro Leu Pro Pro Ser Tyr Val Ala Cys Ser 500 505	1527

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 508 amino acids
  - (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Asp His Leu Gly Ala Ser Leu Trp Pro Gln Val Gly Ser Leu Cys  
1 5 10 15

Leu Leu Leu Ala Gly Ala Ala Trp Ala Pro Pro Pro Asn Leu Pro Asp  
20 25 30

Pro Lys Phe Glu Ser Lys Ala Ala Leu Leu Ala Ala Arg Gly Pro Glu  
35 40 45

Glu Leu Leu Cys Phe Thr Glu Arg Leu Glu Asp Leu Val Cys Phe Trp  
50 55 60

Glu Glu Ala Ala Ser Ala Gly Val Gly Pro Gly Asn Tyr Ser Phe Ser  
65 70 75 80

Tyr Gln Leu Glu Asp Glu Pro Trp Lys Leu Cys Arg Leu His Gln Ala  
85 90 95

Pro Thr Ala Arg Gly Ala Val Arg Phe Trp Cys Ser Leu Pro Thr Ala  
100 105 110

Asp Thr Ser Ser Phe Val Pro Leu Glu Leu Arg Val Thr Ala Ala Ser  
115 120 125

Gly Ala Pro Arg Tyr His Arg Val Ile His Ile Asn Glu Val Val Leu  
130 135 140

Leu Asp Ala Pro Val Gly Leu Val Ala Arg Leu Ala Asp Glu Ser Gly  
145 150 155 160

His Val Val Leu Arg Trp Leu Pro Pro Pro Glu Thr Pro Met Thr Ser  
165 170 175

His Ile Arg Tyr Glu Val Asp Val Ser Ala Gly Asn Gly Ala Gly Ser  
180 185 190

Val Gln Arg Val Glu Ile Leu Glu Gly Arg Thr Glu Cys Val Leu Ser  
195 200 205

Asn Leu Arg Gly Arg Thr Arg Tyr Thr Phe Ala Val Leu Ala Arg Met  
210 215 220

Ala Glu Pro Ser Phe Gly Gly Phe Trp Ser Ala Trp Ser Glu Pro Val  
225 230 235 240

Ser Leu Leu Thr Pro Ser Asp Leu Asp Pro Leu Ile Leu Thr Leu Ser  
245 250 255

Leu Ile Leu Val Val Ile Leu Val Leu Leu Thr Val Leu Ala Leu Leu  
260 265 270

Ser His Arg Arg Ala Leu Lys Gln Lys Ile Trp Pro Gly Ile Pro Ser  
275 280 285

Pro Glu Ser Glu Phe Glu Gly Leu Phe Thr Thr His Lys Gly Asn Phe  
290 295 300

Gln Leu Trp Leu Tyr Gln Asn Asp Gly Cys Leu Trp Trp Ser Pro Cys  
305 310 315 320

Thr Pro Phe Thr Glu Asp Pro Pro Ala Ser Leu Glu Val Leu Ser Glu  
325 330 335

Arg Cys Trp Gly Thr Met Gln Ala Val Glu Pro Gly Thr Asp Asp Glu  
340 345 350

Gly Pro Leu Leu Glu Pro Val Gly Ser Glu His Ala Gln Asp Thr Tyr  
355 360 365

Leu Val Leu Asp Lys Trp Leu Leu Pro Arg Asn Pro Pro Ser Glu Asp  
370 375 380

Leu Pro Gly Pro Gly Gly Ser Val Asp Ile Val Ala Met Asp Glu Gly  
385 390 395 400

Ser Glu Ala Ser Ser Cys Ser Ser Ala Leu Ala Ser Lys Pro Ser Pro  
405 410 415

Glu Gly Ala Ser Ala Ala Ser Phe Glu Tyr Thr Ile Leu Asp Pro Ser  
420 425 430

Ser Gln Leu Leu Arg Pro Trp Thr Leu Cys Pro Glu Leu Pro Pro Thr  
435 440 445

Pro Pro His Leu Lys Tyr Leu Tyr Leu Val Val Ser Asp Ser Gly Ile  
450 455 460

Ser Thr Asp Tyr Ser Ser Gly Asp Ser Gln Gly Ala Gln Gly Gly Leu  
465 470 475 480

Ser Asp Gly Pro Tyr Ser Asn Pro Tyr Glu Asn Ser Leu Ile Pro Ala  
485 490 495

Ala Glu Pro Leu Pro Pro Ser Tyr Val Ala Cys Ser  
500 505